



UTHou-16UTL final.ST25
SEQUENCE LISTING

<110> Board of Regents of the University of Texas System

<120> MUTATIONS IN A NOVEL PHOTORECEPTOR-PINEAL GENE ON 17P CAUSE LEBER
CONGENITAL AMAUROSIS (LCA4)

<130> 96606/16UTL

<140> 09/765,061

<141> 2001-01-17

<150> 60/331362

<151> 2001-01-14

<160> 83

<170> PatentIn version 3.3

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<212> DNA

<213> Homo sapiens

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<221> gene

<222> (1)..(6689)

<223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting
protein-like 1

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<221> misc_feature

<222> (1897)..(1906)

<223> n is a, c, g, or t

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<222> (3946)..(3946)

<223> n is a, c, g, or t

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UTHou-16UTL final.ST25

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UTHou-16UTL final.ST25

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UTHou-16UTL final.ST25

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UTHou-16UTL final.ST25

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UTHou-16UTL final.ST25

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<213> Pan troglodytes

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<223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1

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UTHou-16UTL final.ST25

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 <213> Bos taurus

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UTHou-16UTL final.ST25

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protein-like 1
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<213> Mus musculus

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<222> (1)..(1075)

<223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1

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gaggaggcca aggcggacct ggagaaagtg ctggagttgg agccatccat gcgcaaggcg	900
gtgctcaggg aactgcggct gctggagagc cgcctggcgg acaaacagga ggaggagcgg	960
cagcgctgcc ggagcatgct gggctaggct gggctggatt ccactgagtt agactgggtt	1020
aggttgggtg ggagctgcgg gttgaaccct ggggcgaggg ctggggctat ggact	1075

<210> 7

<211> 1179

<212> DNA

<213> Macaca mulatta

<220>

<221> gene

<222> (1)..(1179)

<223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting protein-like 1

UTHou-16UTL final.ST25

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<400> 7
atggatgccg ctctgctcct gaacgtggaa ggggtcaaga aaaccattct gcacggaggc      60
acgggcgagc tcccaaactt catcaccgga tcccagtgga tctttcattt ccgcaccatg      120
aaatgtgatg aggagcgcac ggtcatcgac gacagccgtc aggtggacca gcccattgcac      180
atcatcatcg ggaacatgtt caagctcgag gtctgggaga tcctgctcac ctccatgagg      240
gtgcacgagg tggccgagtt ctggtgcgac accatccaca cgggggtcta ccccatyctg      300
tcccggagcc tgcggcagat ggcccagggc aaggaccca cggagtggca cgtgcacaca      360
tgcgggctgg ccaacatgtt cgcctaccac acgctgggct acgaggacct ggacgagctg      420
cagaaggagc ctcagcctct gatctttgtg atcgagctgc tgcaggttga cgccccgagt      480
gattaccaga gggagacctg gaacctgagc aatcatgaga agatgaaggt ggtgcccgtc      540
ctccacggag agggaaatcg gctcttcaag ytgggccgct acgaggaggc ctcttccaag      600
taccaggagg ccatcatctg cctaaggaac ctgcagacca aggagaagcc gtgggaggtg      660
cagtggctga agctggagaa gatgatcaac accctgacct tcaactactg ccagtgcctg      720
ctgaagaagg aggagtatta cgagggtgctg gagcacacca gtgacattct ccggcaccac      780
ccaggcatcg tgaaggccta ctatgtgcgt gcccgggctc acgcgagggt gtggaacgag      840
gccgaggcca aggcggacct ccagaaagtg ctggagctgg agccatccat gcagaaggcg      900
gtgcgcaggg agctgaggct gctggagaac cgcattggcg agaagcagga ggaggagagg      960
ctgcgctgcc ggaacatgct gagccaggga gccacgcagc ctcccgaga gccaccggca     1020
cagcccccca cagcaccacc tgcagagctg tccacagggc cacctgcgga cccaccggcg     1080
gagcccccca cagcaccacc tgcggagctg tccacagggc cacctgcaga gccaccggca     1140
gagctcccc tgtccccagg gcactcactg cagcactga                               1179

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<210> 8
<211> 1119
<212> DNA
<213> Saimiri sciureus

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<220>
<221> gene
<222> (1)..(1119)
<223> The AIPL1 gene produces the aryl-hydrocarbon receptor interacting
        protein-like 1

```

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<400> 8
atggatgccg ctctgctcct gaacgtggaa ggggtcaaga agaccattct gcacgggggc      60
acgggcgagc tcccaaattt catcaccgga tcccagtgga tctttcattt ccgcaccatg      120

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UTHou-16UTL final.ST25

aaatgtgatg aggagcggac ggtgattgac gacagcaggg aggtgggcca gcccatgcac	180
atcatcatcg ggaacatggt caagctggag gtctgggaga tcctgctcac gtccatgcgg	240
gtgcgagagg tggccgagtt ctggtgcgac accatccaca cgggggtcta ccccatcctg	300
tcccggagcc tgcggcagat ggcccagggc aaggaccga cgagtgga tgtgcacacg	360
tgcgggctgg ccaacatggt cgcctaccac acgctgggct acgaggacct ggatgagctg	420
cagaaggagc ctcagcctct gatctttgtg atcgagctgc tgcaggttga tgccccaagt	480
gattaccaga gggagacctg gaacctgagc aatcacgaga agatgaagggt ggtgcccgtc	540
ctccatggag aaggaaatag gctcttcaag ctggggcgct acgaggaggc ctcttccaag	600
taccaggagg ccatcatctg cctaaggaac ctgcagacca aggagaaacc ctgggaggtg	660
cagtggctga agctggagaa gatgatcaat accctgatcc tcaactactg tcagtgtctg	720
ctgaagaagg aggagtacta cgaggtcctg gagcatacca gtgacattct ccggcaccac	780
ccaggcattg tgaaggccta ctatgtgcgc gcccgggctc acgcggaggt gtggaacgag	840
gccgaggcca aggcggacct ccagaaagtg ctggagctgg agccgtccat gcagaaggcg	900
gtgcgcaggg agctgaggct gctggagaac cgcattggcg agaagcagga ggaggagcgg	960
ctgcgctgcc gcaacatgct gagccagggg gccacgtggt ccccgcgga gccacccgca	1020
gagccacctg cagagtcac cacagagcca cccgcagagc cacctgcaga gccacctgca	1080
gagctaacct tgaccccggt gcaccacta cagcactga	1119

<210> 9
 <211> 15
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (7)..(9)
 <223> Amino Acid codon position 79: Met to Thr mutation

<400> 9
 acctccacgc gggtg 15

<210> 10
 <211> 15
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (7)..(9)

<223> Amino Acid condon 88 mutation: Trp to X

<400> 10

gagttctgat gcgac

15

<210> 11

<211> 15

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (7)..(9)

<223> Amino Acid condon 96 mutation: Val to Ile mutation

<400> 11

acggggatct acccc

15

<210> 12

<211> 15

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

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<223> Amino Acid codon 124 mutation: Thr to Ile mutation

<400> 12

gaccccatag agtgg

15

<210> 13

<211> 15

<212> DNA

<213> Homo sapiens

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<221> mutation

<222> (7)..(9)

<223> Amino Acid codon 376 mutation: Pro to Ser mutation

<400> 13

ccaccctcgt ccca

15

<210> 14

<211> 15

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

UTHou-16UTL final.ST25

<222> (7)..(9)
 <223> Amino Acid codon 163 mutation: Gln to X mutation

<400> 14
 gattactaga gggag 15

<210> 15
 <211> 15
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (7)..(9)
 <223> Amino Acid codon 197 mutation: Ala to Pro mutation

<400> 15
 gaggagccct cttcc 15

<210> 16
 <211> 15
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (7)..(9)
 <223> Amino Acid codon 278 mutation: Trp to X mutation

<400> 16
 gaggtgtgaa atgag 15

<210> 17
 <211> 15
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (7)..(7)
 <223> a to g mutation: IVS2-2A to G

<400> 17
 tccccacggc acacg 15

<210> 18
 <211> 15
 <212> DNA
 <213> Homo sapiens

<220>

UTHou-16UTL final.ST25

<221> mutation
 <222> (7)..(9)
 <223> Amino Acid codon 262 mutation: Glu to Ser

<400> 18
 cacccaagtg cgcgg 15

<210> 19
 <211> 15
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (7)..(9)
 <223> Amino Acid codon 302 mutation: Arg to Leu

<400> 19
 gcggtgctca gggag 15

<210> 20
 <211> 13
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (5)..(5)
 <223> Deletion of "tgcagagccacc" at location 5

<400> 20
 gccaccaca gca 13

<210> 21
 <211> 15
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (7)..(9)
 <223> Amino Acid codon 239 mutation: Cys to Arg

<400> 21
 tgccagcgcc tgctg 15

<210> 22
 <211> 13
 <212> DNA
 <213> Homo sapiens

UTHou-16UTL final.ST25

<220>
 <221> mutation
 <222> (5)..(5)
 <223> two base deletion at location 5: "ag"

 <400> 22
 tcccgcagcc acc 13

 <210> 23
 <211> 15
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> mutation
 <222> (7)..(9)
 <223> Amino Acid codon 42 mutation: Cys to X

 <400> 23
 atgaaatgag atgag 15

 <210> 24
 <211> 12
 <212> DNA
 <213> Homo sapiens

 <220>
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 <222> (7)..(7)
 <223> nine base deletion at location 7: "ctccggcac"

 <400> 24
 gatattcacc ca 12

 <210> 25
 <211> 21
 <212> DNA
 <213> Homo sapiens

 <220>
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 <222> (7)..(7)
 <223> eight base insertion: "gtgatctt"

 <400> 25
 gactaggtga tcttgtgatc t 21

 <210> 26
 <211> 12
 <212> DNA
 <213> Homo sapiens

UTHou-16UTL final.ST25

<220>
 <221> mutation
 <222> (4)..(4)
 <223> g to a polymorphism: IVS1-9 g to a benign mutation

<400> 26
 ctcagtgact ag 12

<210> 27
 <211> 12
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (4)..(4)
 <223> g to c polymorphism: IVS2+66G to C Benign

<400> 27
 tttgccgggc tg 12

<210> 28
 <211> 12
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (4)..(4)
 <223> c to t polymorphism: IVS2-88C to T Benign

<400> 28
 tcctctcagg ag 12

<210> 29
 <211> 12
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (4)..(4)
 <223> g to a polymorphism: IVS2-14G to A Benign

<400> 29
 atccatttat cc 12

<210> 30
 <211> 12
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (4)..(4)
 <223> a to c mutation: IVS2-10A to C Benign

<400> 30
 cgtttctccc ca 12

<210> 31
 <211> 12
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (4)..(4)
 <223> t to c mutation: IVS3-25T to C Benign

<400> 31
 ctgccccact ga 12

<210> 32
 <211> 12
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (7)..(7)
 <223> t to c mutation: IVS3-21T to C Benign

<400> 32
 cctcaccgac ct 12

<210> 33
 <211> 12
 <212> DNA
 <213> Homo sapiens

<220>
 <221> mutation
 <222> (7)..(7)
 <223> g to a mutation: IVS5+18G to A Benign

<400> 33
 aggagcggac ag 12

<210> 34
 <211> 12
 <212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (7)..(9)

<223> Amino Acid codon mutation: Asp 90 His Benign

<400> 34

tggtgccaca cc

12

<210> 35

<211> 12

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (4)..(6)

<223> Amino Acid mutation: Phe 37 Phe Benign

<400> 35

catttccgca cc

12

<210> 36

<211> 12

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (4)..(6)

<223> Amino Acid mutation: Ser 78 Ser Benign

<400> 36

acctctatgc gg

12

<210> 37

<211> 12

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (4)..(6)

<223> Amino Acid mutation: Cys 89 Cys Benign

<400> 37

tggtgtgaca cc

12

<210> 38

<211> 12

UTHou-16UTL final.ST25

<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(6)
<223> Amino Acid codon mutation: Leu 100 Leu Benign

<400> 38
atcctgtccc gg 12

<210> 39
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(6)
<223> Amino Acid codon mutation: His 172 His

<400> 39
aatcacgaga ag 12

<210> 40
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> mutation
<222> (4)..(6)
<223> Amino Acid codon mutation: Pro 217 Pro Benign

<400> 40
aagccgtggg ag 12

<210> 41
<211> 12
<212> DNA
<213> Homo sapiens

<220>
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<222> (4)..(6)
<223> Amino Acid codon mutation: Asp 255 Asp Benign

<400> 41
agtgacattc tc 12

<210> 42

<211> 20
 <212> DNA
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<220>
 <221> primer
 <222> (1)..(20)
 <223> PCR primer 1 page 57

<400> 42
 aagaaaacca ttctgcacgg 20

<210> 43
 <211> 19
 <212> DNA
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<220>
 <221> primer
 <222> (1)..(19)
 <223> PCR primer 2 page 57

<400> 43
 tgcagctcgt ccaggctcct 19

<210> 44
 <211> 17
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer
 <222> (1)..(17)
 <223> PCR primer 1 page 58

<400> 44
 gacacctccc tttctcc 17

<210> 45
 <211> 18
 <212> DNA
 <213> Homo sapiens

<400> 45
 gctggggctg cctggctg 18

<210> 46
 <211> 20
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(20)
 <223> PCR primer 3 page 58

<400> 46
 ccgagtgatt accagagggga 20

<210> 47
 <211> 20
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(20)
 <223> PCR primer 4 page 58

<400> 47
 tgagctccag cacctcatag 20

<210> 48
 <211> 18
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer
 <222> (1)..(18)
 <223> PCR primer 1 page 60

<400> 48
 acgcagaggt gtggaatg 18

<210> 49
 <211> 19
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer
 <222> (1)..(19)
 <223> PCR primer 2 page 60

<400> 49
 aaaaagtgac accacgatc 19

<210> 50
 <211> 34
 <212> DNA
 <213> Homo sapiens

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<220>
<221> exon
<222> (1)..(34)
<223> exon - donor splice site 1 of Table 1 page 49
      CGGATCCCGAgtgagtggggccctccggagcaga

<400> 50
cgg atc ccg agt gag tgg ggc cct ccg gag cag a      34
Arg Ile Pro Ser Glu Trp Gly Pro Pro Glu Gln
1             5             10

<210> 51
<211> 35
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(35)
<223> exon - acceptor splice site 1 of Table 1 page 49
      cagagtgcaccgtctcggtgactagGTGATCTTTC

<400> 51
cag agt gca ccg tct cgg tga cta ggt gat ctt tc      35
Gln Ser Ala Pro Ser Arg      Leu Gly Asp Leu
1             5             10

<210> 52
<211> 35
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(35)
<223> exon - donor splice site 2 of Table 1 page 49
      CSACACCATCgtaagtaggccctgcgcgcctgtct

<400> 52
csa cac cat cgt aag tag gcc ctg cgc gcc tgt ct      35
Xaa His His Arg Lys      Ala Leu Arg Ala Cys
1             5             10

<210> 53
<211> 35
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(35)

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<223> exon - acceptor splice site 2 of Table 1 page 49

gccatccatccggtttatccccacagCACACGGGGG

<400> 53

gcc atc cat ccg ttt atc ccc aca gca cac ggg gg

35

Ala Ile His Pro Phe Ile Pro Thr Ala His Gly

1 5 10

<210> 54

<211> 35

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(35)

<223> exon - donor splice site 3 of Table 1 page 49

GCTGCTGCAGgtggggctgggggttggcagggctgg

<400> 54

gct gct gca ggt ggg gct ggg gtt ggc agg gct gg

35

Ala Ala Ala Gly Gly Ala Gly Val Gly Arg Ala

1 5 10

<210> 55

<211> 35

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(35)

<223> exon - acceptor splice site 3 of Table 1 page 49

cactgacctgcagctctggggccagGTTGATGCCC

<400> 55

cac tga cct gca gct ctg ggg cca ggt tga tgc cc

35

His Pro Ala Ala Leu Gly Pro Gly Cys

1 5

<210> 56

<211> 35

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(35)

<223> exon - donor splice site 4 of Table 1 page 49

GCAGACCAAGgtcagagggccgctggccacggggtg

<400> 56

gca gac caa ggt cag agg ccg ctg gcc acg ggg tg
Ala Asp Gln Gly Gln Arg Pro Leu Ala Thr Gly
1 5 10

35

<210> 57

<211> 35

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(35)

<223> exon - acceptor splice site 4 of Table 1 page 49

catggctgaccttctccctgggcagGAGAAGCCRT

<400> 57

cat ggc tga cct tct ccc tgg gca gga gaa gcc rt
His Gly Pro Ser Pro Trp Ala Gly Glu Ala
1 5 10

35

<210> 58

<211> 35

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(35)

<223> exon - donor splice site 5 of Table 1 page 49

CACCACCCAGgtgcgcgggggctgcaggggcgga

<400> 58

cac cac cca ggt gcg cgg ggc tgc agg ggc gga ca
His His Pro Gly Ala Arg Gly Cys Arg Gly Gly
1 5 10

35

<210> 59

<211> 35

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (1)..(35)

<223> exon - acceptor splice site 5 of Table 1 page 49

gctggatgctccctgctccccacagGCATCGTGAA

UTHou-16UTL final.ST25

<400> 59
gct gga tgc tcc ctg ctc ccc aca ggc atc gtg aa 35
Ala Gly Cys Ser Leu Leu Pro Thr Gly Ile Val
1 5 10

<210> 60
<211> 18
<212> DNA
<213> Homo sapiens

<220>
<221> primer
<222> (1)..(18)
<223> PCR Primer 1 for AIPL1 fragment amplification Table 5 page 61

<400> 60
ggacacctcc ctttctcc 18

<210> 61
<211> 18
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(18)
<223> PCR Primer 2 for AIPL1 fragment amplification Table 5 page 61

<400> 61
gctggggctg cctggctg 18

<210> 62
<211> 20
<212> DNA
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<220>
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<222> (1)..(20)
<223> PCR Primer 3 for AIPL1 fragment amplification Table 5 page 61

<400> 62
gggccttgaa cagtgtgtct 20

<210> 63
<211> 19
<212> DNA
<213> Homo sapiens

<220>
<221> primer

UTHou-16UTL final.ST25

<222> (1)..(19)
 <223> PCR Primer 4 for AIPL1 fragment amplification Table 5 page 61

<400> 63
 tttcccgaac cacagcagc 19

<210> 64
 <211> 18
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer
 <222> (1)..(18)
 <223> PCR Primer 5 for AIPL1 fragment amplification Table 5 page 61

<400> 64
 agtgaggag caggattc 18

<210> 65
 <211> 20
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(20)
 <223> PCR Primer 6 for AIPL1 fragment amplification Table 5 page 61

<400> 65
 tgcccatgat gcccgctgtc 20

<210> 66
 <211> 18
 <212> DNA
 <213> Homo sapiens

<220>
 <221> PRIMER
 <222> (1)..(18)
 <223> PCR Primer 7 for AIPL1 fragment amplification Table 5 page 61

<400> 66
 tttcgggtct ctgatggg 18

<210> 67
 <211> 17
 <212> DNA
 <213> Homo sapiens

<220>

UTHou-16UTL final.ST25

<221> primer
 <222> (1)..(17)
 <223> PCR Primer 8 for AIPL1 fragment amplification Table 5 page 61
 <400> 67
 gcaggctccc cagagtc 17

<210> 68
 <211> 19
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer
 <222> (1)..(19)
 <223> PCR Primer 9 for AIPL1 fragment amplification Table 5 page 61
 <400> 68
 gcagctgcct caggtcatg 19

<210> 69
 <211> 18
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer
 <222> (1)..(18)
 <223> PCR Primer 10 for AIPL1 fragment amplification Table 5 page 61
 <400> 69
 gtggggtgga aagaaaag 18

<210> 70
 <211> 18
 <212> DNA
 <213> Homo sapiens

<220>
 <221> primer
 <222> (1)..(18)
 <223> PCR Primer 11 for AIPL1 fragment amplification Table 5 page 61
 <400> 70
 ctgggaaggg agctgtag 18

<210> 71
 <211> 19
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(19)
 <223> PCR Primer 12 for AIPL1 fragment amplification Table 5 page 61

<400> 71
 aaaagtgaca ccacgatcc

19

<210> 72
 <211> 384
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1)..(384)
 <223> Human AIPL1 Protein

<400> 72

Met Asp Ala Ala Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
 1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
 20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
 35 40 45

Ile Asp Asp Ser Arg Gln Val Gly Gln Pro Met His Ile Ile Ile Gly
 50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
 65 70 75 80

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
 85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp
 100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
 115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
 130 135 140

Gln Pro Leu Val Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser

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145		150		155		160									
Asp	Tyr	Gln	Arg	Glu	Thr	Trp	Asn	Leu	Ser	Asn	His	Glu	Lys	Met	Lys
				165					170					175	
Ala	Val	Pro	Val	Leu	His	Gly	Glu	Gly	Asn	Arg	Leu	Phe	Lys	Leu	Gly
			180					185					190		
Arg	Tyr	Glu	Glu	Ala	Ser	Ser	Lys	Tyr	Gln	Glu	Ala	Ile	Ile	Cys	Leu
		195					200					205			
Arg	Asn	Leu	Gln	Thr	Lys	Glu	Lys	Pro	Trp	Glu	Val	Gln	Trp	Leu	Lys
	210					215					220				
Leu	Glu	Lys	Met	Ile	Asn	Thr	Leu	Ile	Leu	Asn	Tyr	Cys	Gln	Cys	Leu
225					230					235					240
Leu	Lys	Lys	Glu	Glu	Tyr	Tyr	Glu	Val	Leu	Glu	His	Thr	Ser	Asp	Ile
			245					250						255	
Leu	Arg	His	His	Pro	Gly	Ile	Val	Lys	Ala	Tyr	Tyr	Val	Arg	Ala	Arg
			260					265					270		
Ala	His	Ala	Glu	Val	Trp	Asn	Glu	Ala	Glu	Ala	Lys	Ala	Asp	Leu	Gln
		275					280					285			
Lys	Val	Leu	Glu	Leu	Glu	Pro	Ser	Met	Gln	Lys	Ala	Val	Arg	Arg	Glu
	290					295					300				
Leu	Arg	Leu	Leu	Glu	Asn	Arg	Met	Ala	Glu	Lys	Gln	Glu	Glu	Glu	Arg
305					310					315					320
Leu	Xaa	Cys	Arg	Asn	Met	Leu	Ser	Gln	Gly	Ala	Thr	Gln	Pro	Pro	Ala
				325					330					335	
Glu	Pro	Pro	Thr	Glu	Pro	Pro	Ala	Gln	Ser	Ser	Thr	Glu	Pro	Pro	Ala
			340					345					350		
Glu	Pro	Pro	Thr	Ala	Pro	Ser	Ala	Glu	Leu	Ser	Ala	Gly	Pro	Pro	Ala
		355					360					365			
Glu	Pro	Ala	Thr	Glu	Pro	Pro	Pro	Ser	Pro	Gly	His	Ser	Leu	Gln	His
	370					375					380				

UTHou-16UTL final.ST25

<210> 73
 <211> 384
 <212> PRT
 <213> Pan troglodytes

<220>
 <221> Peptide
 <222> (1)..(384)
 <223> Chimpanzee AIPL1 Protein

<400> 73

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
 1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
 20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
 35 40 45

Ile Asp Asp Ser Arg Gln Val Gly Gln Pro Met His Ile Ile Ile Gly
 50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
 65 70 75 80

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
 85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp
 100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
 115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
 130 135 140

Gln Pro Leu Val Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser
 145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys
 165 170 175

Ala Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
 180 185 190

UTHou-16UTL final.ST25

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Arg
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Ala
325 330 335

Glu Pro Pro Thr Glu Pro Pro Ala Gln Ser Ser Thr Glu Pro Pro Ala
340 345 350

Glu Pro Pro Pro Ala Pro Ser Ala Glu Leu Ser Ala Gly Pro Pro Ala
355 360 365

Glu Thr Ala Thr Glu Pro Pro Pro Ser Pro Gly His Ser Leu Gln His
370 375 380

<210> 74
<211> 372
<212> PRT
<213> Papio anubis

<220>
<221> peptide
<222> (1)..(372)

<223> Baboon AIPL1 Protein

<400> 74

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
 1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
 20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
 35 40 45

Ile Asp Asp Ser Arg Gln Val Asp Gln Pro Met His Ile Ile Ile Gly
 50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
 65 70 75 80

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
 85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp
 100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
 115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
 130 135 140

Gln Pro Leu Ile Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser
 145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys
 165 170 175

Val Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
 180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu
 195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
 210 215 220

UTHou-16UTL final.ST25

Leu Glu Lys Met Ile Asn Thr Leu Thr Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Thr
325 330 335

Glu Pro Pro Ala Glu Pro His Thr Ala Pro Pro Ala Glu Leu Ser Thr
340 345 350

Gly Pro Pro Ala Glu Pro Pro Ala Glu Leu Pro Leu Ser Pro Gly His
355 360 365

Ser Leu Gln His
370

<210> 75
<211> 328
<212> PRT
<213> Bos taurus

<400> 75

Met Asp Ala Thr Leu Leu Leu Asn Val Glu Gly Ile Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Asp Leu Pro Asn Phe Ile Thr Gly Ala Arg
20 25 30

Val Thr Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

UTHou-16UTL final.ST25

Ile Asp Asp Ser Lys Gln Val Gly His Pro Met His Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65 70 75 80

Val Ser Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Glu Gly Lys Asp
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Ile Phe Ile Ile Glu Leu Leu Gln Val Glu Ala Pro Ser
145 150 155 160

Gln Tyr Gln Arg Glu Thr Trp Asn Leu Asn Asn Gln Glu Lys Met Gln
165 170 175

Ala Val Pro Ile Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
180 185 190

Arg Tyr Glu Glu Ala Ser Asn Lys Tyr Gln Glu Ala Ile Val Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Glu
275 280 285

UTHou-16UTL final.ST25

Lys Val Leu Glu Leu Glu Pro Ser Met Arg Lys Ala Val Gln Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Leu Glu Glu Lys Arg Glu Glu Glu Arg
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Gly
325

<210> 76
<211> 328
<212> PRT
<213> Mus musculus

<220>
<221> peptide
<222> (1)..(328)
<223> Mouse AIPL1 Protein

<400> 76

Met Asp Val Ser Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

Val Thr Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Lys Gln Val Gly Gln Pro Met Ser Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Thr Leu Leu Thr Ser Met Arg
65 70 75 80

Leu Gly Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Met Leu Ser Arg Ser Leu Arg Gln Val Ala Glu Gly Lys Asp
100 105 110

Pro Thr Ser Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

UTHou-16UTL final.ST25

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Val Phe Leu Tyr Glu Leu Leu Gln Val Glu Ala Pro Asn
145 150 155 160

Glu Tyr Gln Arg Glu Thr Trp Asn Leu Asn Asn Glu Glu Arg Met Gln
165 170 175

Ala Val Pro Leu Leu His Gly Glu Gly Asn Arg Leu Tyr Lys Leu Gly
180 185 190

Arg Tyr Asp Gln Ala Ala Thr Lys Tyr Gln Glu Ala Ile Val Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Glu Trp Leu Lys
210 215 220

Leu Glu Lys Met Ile Asn Thr Leu Ile Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Met Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Ala Glu Glu Ala Lys Ala Asp Leu Glu
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Arg Lys Ala Val Leu Arg Glu
290 295 300

Leu Arg Leu Leu Glu Ser Arg Leu Ala Asp Lys Gln Glu Glu Glu Arg
305 310 315 320

Gln Arg Cys Arg Ser Met Leu Gly
325

<210> 77
<211> 392
<212> PRT
<213> Macaca mulatta

<220>

UTHou-16UTL final.ST25

<221> peptide

<222> (1)..(392)

<223> Rhesus Monkey AILP1 Protein

<400> 77

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

Val Ile Phe His Phe Arg Thr Met Lys Cys Asp Glu Glu Arg Thr Val
35 40 45

Ile Asp Asp Ser Arg Gln Val Asp Gln Pro Met His Ile Ile Ile Gly
50 55 60

Asn Met Phe Lys Leu Glu Val Trp Glu Ile Leu Leu Thr Ser Met Arg
65 70 75 80

Val His Glu Val Ala Glu Phe Trp Cys Asp Thr Ile His Thr Gly Val
85 90 95

Tyr Pro Ile Leu Ser Arg Ser Leu Arg Gln Met Ala Gln Gly Lys Asp
100 105 110

Pro Thr Glu Trp His Val His Thr Cys Gly Leu Ala Asn Met Phe Ala
115 120 125

Tyr His Thr Leu Gly Tyr Glu Asp Leu Asp Glu Leu Gln Lys Glu Pro
130 135 140

Gln Pro Leu Ile Phe Val Ile Glu Leu Leu Gln Val Asp Ala Pro Ser
145 150 155 160

Asp Tyr Gln Arg Glu Thr Trp Asn Leu Ser Asn His Glu Lys Met Lys
165 170 175

Val Val Pro Val Leu His Gly Glu Gly Asn Arg Leu Phe Lys Leu Gly
180 185 190

Arg Tyr Glu Glu Ala Ser Ser Lys Tyr Gln Glu Ala Ile Ile Cys Leu
195 200 205

Arg Asn Leu Gln Thr Lys Glu Lys Pro Trp Glu Val Gln Trp Leu Lys

UTHou-16UTL final.ST25

210

215

220

Leu Glu Lys Met Ile Asn Thr Leu Thr Leu Asn Tyr Cys Gln Cys Leu
225 230 235 240

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Gln Pro Pro Ala
325 330 335

Glu Pro Pro Ala Gln Pro Pro Thr Ala Pro Pro Ala Glu Leu Ser Thr
340 345 350

Gly Pro Pro Ala Asp Pro Pro Ala Glu Pro Pro Thr Ala Pro Pro Ala
355 360 365

Glu Leu Ser Thr Gly Pro Pro Ala Glu Pro Pro Ala Glu Leu Pro Leu
370 375 380

Ser Pro Gly His Ser Leu Gln His
385 390

<210> 78
<211> 372
<212> PRT
<213> Saimiri sciureus

<220>
<221> peptide
<222> (1)..(372)
<223> Squirrel Monkey AIPL1 Protein

<400> 78

UTHou-16UTL final.ST25

Met	Asp	Ala	Ala	Leu	Leu	Leu	Asn	Val	Glu	Gly	Val	Lys	Lys	Thr	Ile	1	5	10	15
Leu	His	Gly	Gly	Thr	Gly	Glu	Leu	Pro	Asn	Phe	Ile	Thr	Gly	Ser	Arg	20	25	30	
Val	Ile	Phe	His	Phe	Arg	Thr	Met	Lys	Cys	Asp	Glu	Glu	Arg	Thr	Val	35	40	45	
Ile	Asp	Asp	Ser	Arg	Glu	Val	Gly	Gln	Pro	Met	His	Ile	Ile	Ile	Gly	50	55	60	
Asn	Met	Phe	Lys	Leu	Glu	Val	Trp	Glu	Ile	Leu	Leu	Thr	Ser	Met	Arg	65	70	75	80
Val	Arg	Glu	Val	Ala	Glu	Phe	Trp	Cys	Asp	Thr	Ile	His	Thr	Gly	Val	85	90	95	
Tyr	Pro	Ile	Leu	Ser	Arg	Ser	Leu	Arg	Gln	Met	Ala	Gln	Gly	Lys	Asp	100	105	110	
Pro	Thr	Glu	Trp	His	Val	His	Thr	Cys	Gly	Leu	Ala	Asn	Met	Phe	Ala	115	120	125	
Tyr	His	Thr	Leu	Gly	Tyr	Glu	Asp	Leu	Asp	Glu	Leu	Gln	Lys	Glu	Pro	130	135	140	
Gln	Pro	Leu	Ile	Phe	Val	Ile	Glu	Leu	Leu	Gln	Val	Asp	Ala	Pro	Ser	145	150	155	160
Asp	Tyr	Gln	Arg	Glu	Thr	Trp	Asn	Leu	Ser	Asn	His	Glu	Lys	Met	Lys	165	170	175	
Val	Val	Pro	Val	Leu	His	Gly	Glu	Gly	Asn	Arg	Leu	Phe	Lys	Leu	Gly	180	185	190	
Arg	Tyr	Glu	Glu	Ala	Ser	Ser	Lys	Tyr	Gln	Glu	Ala	Ile	Ile	Cys	Leu	195	200	205	
Arg	Asn	Leu	Gln	Thr	Lys	Glu	Lys	Pro	Trp	Glu	Val	Gln	Trp	Leu	Lys	210	215	220	
Leu	Glu	Lys	Met	Ile	Asn	Thr	Leu	Ile	Leu	Asn	Tyr	Cys	Gln	Cys	Leu	225	230	235	240

UTHou-16UTL final.ST25

Leu Lys Lys Glu Glu Tyr Tyr Glu Val Leu Glu His Thr Ser Asp Ile
245 250 255

Leu Arg His His Pro Gly Ile Val Lys Ala Tyr Tyr Val Arg Ala Arg
260 265 270

Ala His Ala Glu Val Trp Asn Glu Ala Glu Ala Lys Ala Asp Leu Gln
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Gln Lys Ala Val Arg Arg Glu
290 295 300

Leu Arg Leu Leu Glu Asn Arg Met Ala Glu Lys Gln Glu Glu Glu Arg
305 310 315 320

Leu Arg Cys Arg Asn Met Leu Ser Gln Gly Ala Thr Trp Ser Pro Ala
325 330 335

Glu Pro Pro Ala Glu Pro Pro Ala Glu Ser Ser Thr Glu Pro Pro Ala
340 345 350

Glu Pro Pro Ala Glu Pro Pro Ala Glu Leu Thr Leu Thr Pro Gly His
355 360 365

Pro Leu Gln His
370

<210> 79
<211> 328
<212> PRT
<213> Rattus norvegicus

<220>
<221> PEPTIDE
<222> (1)..(328)
<223> AIPL1 Protein rat - from Figure 1

<400> 79

Met Asp Ala Ala Leu Leu Leu Asn Val Glu Gly Val Lys Lys Thr Ile
1 5 10 15

Leu His Gly Gly Thr Gly Glu Leu Pro Asn Phe Ile Thr Gly Ser Arg
20 25 30

Val	Thr	Phe	His	Phe	Arg	Thr	Met	Lys	Cys	Asp	Glu	Glu	Arg	Thr	Val
		35					40					45			
Ile	Asp	Asp	Ser	Lys	Gln	Val	Gly	Gln	Pro	Met	Asn	Ile	Ile	Ile	Gly
	50					55					60				
Asn	Met	Phe	Lys	Leu	Glu	Val	Trp	Glu	Ile	Leu	Leu	Thr	Ser	Met	Arg
65					70					75					80
Leu	Gly	Glu	Val	Ala	Glu	Phe	Trp	Cys	Asp	Thr	Ile	His	Thr	Gly	Val
				85					90					95	
Tyr	Pro	Met	Leu	Ser	Arg	Ser	Leu	Arg	Gln	Val	Ala	Glu	Gly	Lys	Asp
			100					105					110		
Pro	Thr	Ser	Trp	His	Val	His	Thr	Cys	Gly	Leu	Ala	Asn	Met	Phe	Ala
		115					120					125			
Tyr	His	Thr	Leu	Gly	Tyr	Glu	Asp	Leu	Asp	Glu	Leu	Gln	Lys	Glu	Pro
	130					135					140				
Gln	Pro	Leu	Ile	Phe	Leu	Ile	Glu	Leu	Leu	Gln	Val	Glu	Ala	Pro	Asn
145					150					155					160
Glu	Tyr	Gln	Arg	Glu	Thr	Trp	Asn	Leu	Asn	Asn	Glu	Glu	Arg	Met	Gln
				165					170					175	
Ala	Val	Pro	Leu	Leu	His	Gly	Glu	Gly	Asn	Arg	Leu	Tyr	Lys	Leu	Gly
			180					185					190		
Arg	Tyr	Asp	Gln	Ala	Ala	Thr	Lys	Tyr	Gln	Glu	Ala	Ile	Ile	Cys	Leu
		195					200					205			
Arg	Asn	Leu	Gln	Thr	Lys	Glu	Lys	Pro	Trp	Glu	Val	Glu	Trp	Leu	Lys
	210					215					220				
Leu	Glu	Lys	Met	Ile	Asn	Thr	Leu	Ile	Leu	Asn	Tyr	Cys	Gln	Cys	Leu
225					230					235					240
Leu	Lys	Lys	Glu	Glu	Tyr	Tyr	Glu	Val	Leu	Glu	His	Thr	Ser	Asp	Ile
				245					250					255	
Leu	Arg	His	His	Pro	Gly	Ile	Val	Lys	Ala	Tyr	Tyr	Met	Arg	Ala	Arg
			260					265					270		

UTHou-16UTL final.ST25

Ala His Ala Glu Val Trp Asn Ala Glu Glu Ala Lys Ala Asp Leu Glu
275 280 285

Lys Val Leu Glu Leu Glu Pro Ser Met Arg Lys Ala Val Leu Arg Glu
290 295 300

Leu Arg Leu Leu Glu Ser Arg Leu Ala Asp Lys Gln Glu Glu Glu Arg
305 310 315 320

Gln Arg Cys Arg Ser Met Leu Gly
325

<210> 80
<211> 330
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(330)
<223> AIP Protein human - From Figure 1

<400> 80

Met Ala Asp Ile Ile Ala Arg Leu Arg Glu Asp Gly Ile Gln Lys Arg
1 5 10 15

Val Ile Gln Glu Gly Arg Gly Glu Leu Pro Asp Phe Gln Asp Gly Thr
20 25 30

Lys Ala Thr Phe His Tyr Arg Thr Leu His Ser Asp Asp Glu Gly Thr
35 40 45

Val Leu Asp Asp Ser Arg Ala Arg Gly Lys Pro Met Glu Leu Ile Ile
50 55 60

Gly Lys Lys Phe Lys Leu Pro Val Trp Glu Thr Ile Val Cys Thr Met
65 70 75 80

Arg Glu Gly Glu Ile Ala Gln Phe Leu Cys Asp Ile Lys His Val Val
85 90 95

Leu Tyr Pro Leu Val Ala Lys Ser Leu Arg Asn Ile Ala Val Gly Lys
100 105 110

Asp Pro Leu Glu Gly Gln Arg His Cys Cys Gly Val Ala Gln Met Arg

UTHou-16UTL final.ST25

115

120

125

Glu His Ser Ser Leu Gly His Ala Asp Leu Asp Ala Leu Gln Gln Asn
130 135 140

Pro Gln Pro Leu Ile Phe His Met Glu Met Leu Lys Val Glu Ser Pro
145 150 155 160

Gly Thr Tyr Gln Gln Asp Pro Trp Ala Met Thr Asp Glu Glu Lys Ala
165 170 175

Lys Ala Val Pro Leu Ile His Gln Glu Gly Asn Arg Leu Tyr Arg Glu
180 185 190

Gly His Val Lys Glu Ala Ala Ala Lys Tyr Tyr Asp Ala Ile Ala Cys
195 200 205

Leu Lys Asn Leu Gln Met Lys Glu Gln Pro Gly Ser Pro Glu Trp Ile
210 215 220

Gln Leu Asp Lys Gln Ile Thr Pro Leu Leu Leu Asn Tyr Cys Gln Cys
225 230 235 240

Lys Leu Val Val Glu Glu Tyr Tyr Glu Val Leu Asp His Cys Ser Ser
245 250 255

Ile Leu Asn Lys Tyr Asp Asp Asn Val Lys Ala Tyr Phe Lys Arg Gly
260 265 270

Lys Ala His Ala Ala Val Trp Asn Ala Gln Glu Ala Gln Ala Asp Phe
275 280 285

Ala Lys Val Leu Glu Leu Asp Pro Ala Leu Ala Pro Val Val Ser Arg
290 295 300

Glu Leu Arg Ala Leu Glu Ala Arg Ile Arg Gln Lys Asp Glu Glu Asp
305 310 315 320

Lys Ala Arg Phe Arg Gly Ile Phe Ser His
325 330

<210> 81

<211> 330

<212> PRT

<213> Mus musculus

UTHou-16UTL final.ST25

<220>

<221> PEPTIDE

<222> (1)..(330)

<223> AIP Protein mouse - From Figure 1

<400> 81

Met Ala Asp Leu Ile Ala Arg Leu Arg Glu Asp Gly Ile Gln Lys Arg
1 5 10 15

Val Ile Gln Glu Gly Arg Gly Glu Leu Pro Asp Phe Gln Asp Gly Thr
20 25 30

Lys Ala Thr Phe His Phe Arg Thr Leu His Ser Asp Asn Glu Gly Ser
35 40 45

Val Ile Asp Asp Ser Arg Thr Arg Gly Lys Pro Met Glu Leu Ile Val
50 55 60

Gly Lys Lys Phe Lys Leu Pro Val Trp Glu Thr Ile Val Cys Thr Met
65 70 75 80

Arg Glu Gly Glu Ile Ala Gln Phe Leu Cys Asp Ile Lys His Val Val
85 90 95

Leu Tyr Pro Leu Val Ala Lys Ser Leu Arg Asn Ile Ala Glu Gly Lys
100 105 110

Asp Pro Leu Glu Gly Gln Arg His Cys Cys Gly Ile Ala Gln Met His
115 120 125

Glu His Ser Ser Leu Gly His Ala Asp Leu Asp Ala Leu Gln Gln Asn
130 135 140

Pro Gln Pro Leu Ile Phe His Ile Glu Met Leu Lys Val Glu Ser Pro
145 150 155 160

Gly Thr Tyr Gln Gln Asp Pro Trp Ala Met Thr Asp Glu Glu Lys Ala
165 170 175

Lys Ala Val Pro Val Ile His Gln Glu Gly Asn Arg Leu Tyr Arg Glu
180 185 190

Gly Gln Val Lys Glu Ala Ala Ala Lys Tyr Tyr Asp Ala Ile Ala Cys
195 200 205

UTHou-16UTL final.ST25

Leu Lys Asn Leu Gln Met Lys Glu Gln Pro Gly Ser Pro Asp Trp Ile
210 215 220

Gln Leu Asp Leu Gln Ile Thr Pro Leu Leu Leu Asn Tyr Cys Gln Cys
225 230 235 240

Lys Leu Val Ala Gln Glu Tyr Tyr Glu Val Leu Asp His Cys Ser Ser
245 250 255

Ile Leu Asn Lys Tyr Asp Asp Asn Val Lys Ala Tyr Phe Lys Arg Gly
260 265 270

Lys Ala His Ala Ala Val Trp Asn Ala Gln Glu Ala Gln Ala Asp Phe
275 280 285

Ala Lys Val Leu Glu Leu Asp Pro Ala Leu Ala Pro Val Val Ser Arg
290 295 300

Glu Leu Arg Ala Leu Glu Thr Arg Ile Arg Gln Lys Asp Glu Glu Asp
305 310 315 320

Lys Ala Arg Phe Arg Gly Ile Phe Ser His
325 330

<210> 82
<211> 8
<212> DNA
<213> Homo sapiens

<220>
<221> misc_structure
<222> (1)..(8)
<223> Eight Base insertion as Val 33 in the AIPL1 gene

<400> 82
gtgatctt

8

<210> 83
<211> 9
<212> DNA
<213> Homo sapiens

<220>
<221> misc_structure
<222> (1)..(9)
<223> Nine base deletion at Leu 257 of the AIPL1 gene

UTHou-16UTL final.ST25

<400> 83
ctccggcac

9